REMARKS

In an Office Action mailed March 25, 2005, the Examiner noted Applicants' election of the Claims of Group I, and withdrew Claims 9-18 from further consideration. The Examiner objected to Figure 1 for failing to comply with the requirements for disclosures reciting nucleic acid sequences. The Examiner rejected Claims 1-8. Claims 1, 3 and 5-8 were rejected under §112, first paragraph for failing to adequately describe claimed subject matter in the Specification. Claim 3 was rejected under §112, second paragraph for failing to define a term in the Specification. Claims 1-2 and 4-5 were rejected under section 102(b) as being anticipated by Reznikoff WS, *The Tn5 Transposon*, Ann. Rev. Microbiol. 47:945-963 (1993).

The Applicants respond to each of the Examiner's objections and rejections below. In view of the amendments noted above and the arguments presented herein, the Applicants respectfully request reconsideration of the merits of this application.

Objection for failing to comply with 37 C.F.R. §§ 1.821-1.825

The Examiner objected to the drawings, alleging that the application failed to comply with the requirements for identifying nucleotide sequences as set forth in 37 C.F.R. §§ 1.821-1.825. The Applicants direct the Examiner's attention to paragraph [0043] of the Specification as filed which includes the requested information. Nevertheless, in the interest of expediting prosecution, Applicants amend paragraph [0022] to list the sequence identifiers associated with the nucleotide sequences disclosed in Figure 1. Applicants believe that the application complies with the requirements set forth in 37 C.F.R. §§ 1.821-1.825 and respectfully request reconsideration of the objection as applied to the above-identified drawings.

Rejections Under § 112, First Paragraph

The Examiner rejected Claims 1, 3 and 5-8 under 35 U.S.C. § 112, first paragraph, alleging that the Specification failed to adequately describe a broad class of polynucleotides comprising inverted repeat sequence pairs of any sequence or of any Tn5 mosaic end sequence and because the Specification failed to disclose a structure-function analysis of the Tn5 sequences. The Examiner further alleged that the Specification does not provide guidance on the essential regions of the polynucleotides that could be modified and retain function. The Applicants respectfully disagree.

First, Tn5 inverted sequence pair analysis and structure-function analysis were well known to those skilled in the relevant art at the time the above-identified application was filed. For example, the base pair sequences of the inverted end repeats (both OE and IE) were previously reported as nineteen base pairs. *See* Zhou M & Reznikoff WS, *Tn5 transposase mutant that alter DNA binding specificity*, J. Mol. Biol. 271:362-373 (1997); *see also* Zhou M, et al., *Molecular genetic analysis of transposase-end DNA sequence recognition: cooperativity of three adjacent base-pairs in specific interaction with a mutant Tn5 transposase*, J. Mol. Biol. 276:913-925 (1998). Additionally, the sequences of the nineteen base pairs of the inverted end repeats were previously reported to have twelve identical and seven non-identical base pairs. *See id.* Specifically, the OE sequence was reported as CTGACTCTTATACACAAGT; and the IE sequence was reported as CTGTCTCTTGATCAGATCT (the seven non-identical base pairs are underlined). *See id.*

Zhou et al., *supra*, also discloses an elaborate study of an inverted end repeat containing either the OE nucleotide pair or the IE nucleotide pair at each of the seven non-identical positions between the OE and the IE. Because there was a total of 2^7 or 128 different mutants that could exist, the authors estimated that there was less than a 5% chance that they could have missed examining any of the 128 possible mutants. In table 1, Zhou et al. discloses the results of the favorable and unfavorable inverted end repeat mutants. For example, table 1 shows that IE inverted end repeats with OE nucleotide pairs at positions 10-12 resulted in a favorable interaction with either a Tn5 mutant transposase or a wild-type transposase (see Figure 4). Furthermore, Zhou et al. discloses that IE inverted end repeats with OE nucleotides at position 4 or position 18 may adversely affect Tn5-mediated transposition. As such, one with skill in the relevant art would possess the required knowledge of Tn5 OE and IE sequence pair analysis and structure-function analysis to practice the invention disclosed in the above-identified application.

U.S. Patent No. 6,406,896 and U.S. Patent No. 5,965,443, both cited by the Examiner in a section 102(b) rejection discussed below, disclose information relevant to the structure-function relationship of the Tn5 transposase and the OE and IE sequences. The '896 patent, for example, discloses modifications to a wild-type Tn5 transposase to increase its binding preference to the IE sequence over the OE sequence which it normally prefers. Likewise, the '443 patent discloses modifications to a wild-type Tn5 transposase to increase even more its binding preference to the OE sequence.

Second, Tn5 mosaic end (ME) sequences were also well known to one skilled in the relevant art at the time the above-identified application was filed. The basic parts of the ME sequences are disclosed by Zhou et al., which makes clear that ME sequences are a hybrid of the OE and IE sequences, preferable containing the OE nucleotides at positions 10-12. Additionally, Bhasin A, et al., *Hairpin formation in Tn5 transposition*, J. Biol. Chem. 274:37021-37029 (1999) defines the ME sequence as "a hyperactive, synthetic and sequence that is a hybrid of the OE and IE." Bhasin et al. also disclose an example of the ME sequence – an IE sequence containing the OE nucleotides at positions 10-12, which is identical in sequence to Linker B of Figure 1 in the above-identified application. As such, one with skill in the relevant art would have possessed the required knowledge of ME sequences to practice the invention disclosed in the above-identified application when it was filed. The Applicants believe that OE, IE and ME sequences were described in the Specification of the above-identified application with sufficient detail to permit a skilled artisan to practice the claimed invention. Accordingly, the Applicants respectfully request reconsideration of the rejection as applied to Claims 1, 3 and 5-8.

Rejections Under § 112, Second Paragraph

The Examiner rejected Claim 3 under 35 U.S.C. § 112, second paragraph, alleging that the phrase "Tn5 mosaic end sequences" is vague and indefinite. The Applicants respectfully disagree.

As discussed above, mosaic end sequences were known to those skilled in the relevant art at the time the above-identified application was filed. One with skill in the relevant art would not have required a definition of Tn5 mosaic end sequences to practice the invention disclosed in the above-identified application. Thus, the Applicants believe that mosaic end sequences were adequately described in the Specification of the above-identified application and respectfully request reconsideration of the rejection as applied to Claim 3.

Rejections Under § 102(b)

The Examiner rejected Claims 1-2 and 4-5 under 35 U.S.C. § 102(b), alleging that each was anticipated by Reznikoff WS, *The Tn5 transposase*, Annu. Rev. Microbiol. 47:945-963 (1993). Applicants respectfully traverse the rejection in view of the amendments to Claim 1. Claim 1 recites that the polynucleotide includes a sequence that confers selectability upon a host cell, where the sequence is positioned directly between members of

distinct repeat sequence pairs. In other words, the closest inverted repeat sequences flanking (i.e., to the 5' and to the 3' side of) the selectability-conferring sequence are not members of the same repeat sequence pair, but instead are members of different pairs. The claims do not require the flanking members to be directly adjacent to or continguous with the selectability-conferring sequence. The Applicants find support for this amendment in paragraph [0049] and Figures 2, 4-5 and 7-9.

While Reznikoff discloses the basic structure of the Tn5 transposon, the selectability-conferring sequence of Tn5 transposon is positioned directly between the first and second members of one inverted repeat sequence pair (the IE sequences), rather than at the position recited in amended Claim 1. Therefore, Reznikoff cannot anticipate amended Claim 1. Applicants respectfully request reconsideration of this rejection as applied to Claim 1 and dependent Claims 2 and 4-5.

For the sake of completeness, neither U.S. Patent No. 6,406,896 or U.S. Patent No. 5,965,443, cited by the Examiner for their disclosure of specificity of certain transposase enzymes, discloses such a structure either.

Additional Remarks

The Applicants amend Claims 5 and 6 to reflect the amendments to Claim 1. The Applicants find support for these amendments in Figures 4-5 and 7-9.

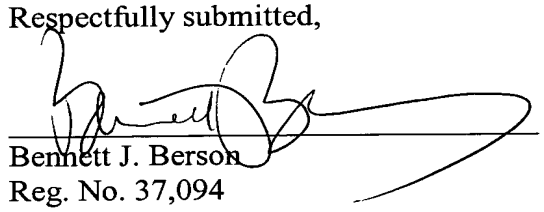
Additionally, the Applicants respectfully request that non-elected Claims 9-18 be cancelled without prejudice to the filing of a divisional application.

Fees

A petition for a one-month extension of time to Monday, July 25, 2005, accompanies this response so the response will be deemed to have been timely filed. Please charge the appropriate extension fee due to Deposit Account No. 17-0055. Should any additional extension of time be due in this or any subsequent response, please consider this to be a petition for the appropriate extension of time and a request to charge the fee due to the same deposit account.

No other fee is believed due in connection with this submission. However, if an additional fee is due in this or any subsequent response, please charge the fee to this same deposit account.

Respectfully submitted,



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